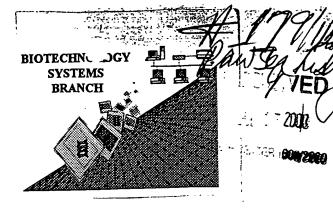
RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

08/986,60

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

SERIAL NUMBER:

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE _ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces. . : The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs Misaligned Amino Acid Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers. Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Variable Length __ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid Patentin ver. 2.0 "bug" . Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. missing. If intentional, please use the following format for each skipped sequence: **Skipped Sequences** Sequence(s) (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). **Skipped Sequences** Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Use of <213>Organism Sequence(s) are missing this mandatory field or its response. (NEW RULES) Use of <220>Feature _ are missing the <220>Feature and associated headings. Sequence(s) (NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) Patentin ver. 2.0 "bug" Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.



JE 17 200

1653

TECH CENTER 1600/2900

Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/986,606B

DATE: 07/11/2000 Joseph Server Jummary

Does Not Comply

Scried Diskette No. TIME: 10:35:46

Input Set : A:\ES.txt

Output Set: N:\CRF3\07112000\H986606B.raw

4 <110> APPLICANT: Sloane, Nathan H

6 Sixteen Amino Acid of the Antineoplastic Protein (ANUP)

6 <112> Sixteen Amino Acid of the Antineoplastic Protein (ANUP)

as a Pharmaceutically Active Anti-Tumor Agent

W--> 0 <120> TITLE INVENTION:

W--> 0 <130> FILE REFERENCE:

9 <140> CURRENT APPLICATION NUMBER: US 08/986,606B

11 <141> CURRENT FILING DATE: 1997-12-8

W--> 13 <150> PRIOR APPLICATION NUMBER:

W--> 15 <151> PRIOR FILING DATE:

17 <160> NUMBER OF SEQ ID NOS: 1

20 <170> SOFTWARE: PatentIn ver. 2.0

ERRORED SEQUENCES

E--> 23 <210> SEQ ID NO: Seq ID No: #1

25 <211> LENGTH: 16

27 <212> TYPE: PRT

29 <213> ORGANISM: Artificial Sequence

W--> 31 <220> FEATURE: Xaa is -N-Terminal pyroglutamyl (pyroGLU)

W--> 33 <221> NAME/KEY:

35 <222> LOCATION: 1 37 <223> OTHER INFORMATION: Xaa is pyroGLU

E--> 39 <400> SEQUENCE: 1

41 Xaa LEV LYS CYS TYR THR CYS LYS GLU PRO 10

E--> 42 MET THR SER ALA ALA CYS

All next page

RECEIVED

JUL 172000

TECH CENTER 1000 (ESC)

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/986,606B

Input Set : A:\ES.txt

Output Set: N:\CRF3\07112000\H986606B.raw

DATE: 07/11/2000

TIME: 10:35:47

L:6 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:11 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:13 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:31 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:39 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:42 M:252 E: No. of Seq. differs, <211>LENGTH:Input:16 Found:0 SEQ:0

\$ /986,606B

SEQUENCE LISTING

delite- not used under new Seguere Rules

<110> Sloane, Nathan H

<112> Sixteen Amino Acid of the Antineoplastic Protein (ANUP) 2/207 as a Pharmaceutically Active Anti-Tumor Agent

<140> US 08/986,606

<141> 1997-12-8

<150>

- delete if he response que

<160> 1

<170> PatentIn ver. 2.0

<210> (Seq ID No: #)1

<211> 16

<212> PRT

I All Lem 12 on Ever Summery Steet <213×Artificial Sequence

<220> (Xaa is -N-Terminal pyroglutamy) (pyrogLU) more love - 62207 los ho

<221>

<222> 1

<223> Xaa is pyroGLU

response. It is a Lesder only.

<400> 1 Juli

Xaa (LEV) LYS CYS TYR THR CYS LYS GLU PRO

MET THR SER ALA ALA CYS

(10) delete are numbered cumulatively at end of line.

number ameis outs wider every 5 anord auds. DO NOT use TABS = between amind overli. Use space

characters